

Length Frequency and Proportional Size Distribution (PSD) of Largemouth Bass 2014-2017

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Data Preparation

```
# PSD <-  
# read.csv('Data/Clean-Data/2012-2017_nearshore-survey-largemouth-bass_Stock_CLEAN.csv')  
# %>%  
PSD <- read.csv("Data/Clean-Data/largemouth-bass_Wr_Stock.csv") %>% arrange(Year,  
  FID, Length)  
PSD$fyrr <- as.factor(PSD$fyrr)  
  
str(PSD)  
  
## 'data.frame': 445 obs. of 13 variables:  
## $ fyrr : Factor w/ 5 levels "13","14","15",...: 1 1 1 1 1 1 1 1 1 1 ...  
## $ Year : int 2013 2013 2013 2013 2013 2013 2013 2013 2013 2013 ...  
## $ Site : int 11 11 11 11 11 11 11 10 10 10 ...  
## $ FID : int 1 2 3 4 6 7 8 9 10 17 ...  
## $ Weight: int 968 604 273 160 350 316 1159 807 302 370 ...  
## $ Ws : num 935 617 256 146 460 ...  
## $ Wr : num 103.6 97.8 106.5 109.6 76.1 ...  
## $ Length: int 395 348 266 224 318 273 426 387 264 291 ...  
## $ lcat20: int 380 340 260 220 300 260 420 380 260 280 ...  
## $ gcat : Factor w/ 3 levels "preferred","quality",...: 1 2 3 3 2 3 1 1 3 3 ...  
## $ Age : int 3 2 1 1 2 1 3 4 1 1 ...  
## $ SexCon: int 3 8 8 6 8 8 3 8 3 8 ...  
## $ Sex : int 1 2 2 2 2 2 1 2 1 2 ...  
  
# headtail(PSD)  
unique(PSD$Year) ### See that there is no year 2012  
  
## [1] 2013 2014 2015 2016 2017  
  
{ Create length bins, tidy=TRUE, results='hide'} PSD %>% mutate(lcat20=lencat(Length,w=20));  
headtail(PSD) ### just looking at data PSD[c(400:447),c(1,3,5,16,17)]  
  
psd.13 <- filter(PSD, Year == 2013)  
psd.14 <- filter(PSD, Year == 2014)  
psd.15 <- filter(PSD, Year == 2015)  
psd.16 <- filter(PSD, Year == 2016)  
# psd.17 <- filter(PSD, Year==2017)
```

My plan is to make a data file with the PSD of Preferred and Quality length largemouth bass for each year (2013 - 2017). This will be used for comparison graph against Relative weight and should provide some insight into whether the population is experiencing slow growth (perhaps due to competition for resources) or excessive mortality (perhaps due to overfishing). Both of these things can affect the proportion of large individuals and thus angler satisfaction and may be correctable with regulatory changes.

Possible conclusions about the status of the population (Guy and Brown pg 412).

- 1) **Poor Habitat** low recruitment, slow growth, and moderate to high mortality due to poor habitat.
- 2) **Overharvest** of largemouth bass greater than quality length (or maybe preferred).
- 3) **Stunting** high density of small, slow-growing largemouth bass due to excessive recruitment resulting in stunted growth due to excessive intraspecific competition at young ages.

Note I am not using data from 2012 because of differences in the data collection procedures. Only large fish were measures weighed and aged all others were just counted.

Note data from 2013 does not have and weight associated with it (Due to the lack of an individual identification variable and the seperation of length and weight on two tabs in the excell sheet). so 2013 will not be used for the graph of Wr and PSD.

Calculate PSD-X and 95% CI 2013 - 2017

```
### 2013
(PSD_CI_13 <- psdCalc(~Length, data = psd.13, species = "Largemouth Bass", what = "traditional"))

## Warning: Some category sample size <20, some CI coverage may be
## lower than 95%.

##      Estimate 95% LCI 95% UCI
## PSD-Q      58      45      70
## PSD-P      16       7      26

# save(PSD_CI_13,file = 'model-output/PSD_CI_13.rda')

### 2014
(PSD_CI_14 <- psdCalc(~Length, data = psd.14, species = "Largemouth Bass", what = "traditional"))

## Warning: Some category sample size <20, some CI coverage may be
## lower than 95%.

##      Estimate 95% LCI 95% UCI
## PSD-Q      54      43      64
## PSD-P      13       6      20

# save(PSD_CI_14,file = 'model-output/PSD_CI_14.rda')

### 2015
(PSD_CI_15 <- psdCalc(~Length, data = psd.15, species = "Largemouth Bass", what = "traditional"))

## Warning: Some category sample size <20, some CI coverage may be
## lower than 95%.

##      Estimate 95% LCI 95% UCI
## PSD-Q      79      67      91
## PSD-P      22      10      35
```

```
# save(PSD_CI_15,file = 'model-output/PSD_CI_15.rda')

### 2016
(PSD_CI_16 <- psdCalc(~Length, data = psd.16, species = "Largemouth Bass", what = "traditional"))

## Warning: Some category sample size <20, some CI coverage may be
## lower than 95%.

##      Estimate 95% LCI 95% UCI
## PSD-Q      51      39      63
## PSD-P       9       2      16

# save(PSD_CI_16,file = 'model-output/PSD_CI_16.rda')

### 2017 (PSD_CI_17 <- psdCalc(~Length, data=psd.17, species = 'Largemouth
### Bass', what = 'traditional')) save(PSD_CI_17,file =
### 'model-output/PSD_CI_17.rda')
```

Notice

Warning message: Some category sample size <20, some CI coverage may be lower than 95%.

Create Data Frame containing PSD-X and 95% CI for all years 2013 - 2017

```
(psd.Q <- rbind(PSD_CI_13["PSD-Q",],
               PSD_CI_16["PSD-Q",],
               PSD_CI_15["PSD-Q",],
               PSD_CI_16["PSD-Q",]))
```

```
##      Estimate 95% LCI 95% UCI
## [1,]      58      45      70
## [2,]      51      39      63
## [3,]      79      67      91
## [4,]      51      39      63
```

```
Years <- c("2013", "2014", "2015", "2016")
```

```
PSD.Q <- data.frame(Years,psd.Q)
names(PSD.Q) <- c("Years", "PSD-Q", "LCI", "UCI")
PSD.Q
```

```
##   Years PSD-Q LCI UCI
## 1  2013   58  45  70
## 2  2014   51  39  63
## 3  2015   79  67  91
## 4  2016   51  39  63
```

```
#1-30-2018#write.csv(PSD.Q, file="Data/Clean-Data/PSD-Q.csv",row.names = FALSE)
```

```
(psd.P <- rbind(PSD_CI_13["PSD-P",],
               PSD_CI_16["PSD-P",],
               PSD_CI_15["PSD-P",],
               PSD_CI_16["PSD-P",]))
```

```
##      Estimate 95% LCI 95% UCI
## [1,]      16       7      26
```

```
## [2,]      9      2     16
## [3,]     22     10     35
## [4,]      9      2     16
```

```
Years <- c("2013", "2014", "2015", "2016")
```

```
PSD.P <- data.frame(Years,psd.P)
names(PSD.P) <- c("Years", "PSD-P", "LCI", "UCI")
PSD.P
```

```
##   Years PSD-P LCI UCI
## 1  2013    16   7  26
## 2  2014     9   2  16
## 3  2015    22  10  35
## 4  2016     9   2  16
```

```
#1-30-2018#write.csv(PSD.P, file="Data/Clean-Data/PSD-P.csv", row.names = FALSE)
```

New .csv saved in Clean-Data.

```
%%%%%%%%%%%
```

Below Everything is Redundant

I created new .rmd files to separate the steps of the analysis below in order to make everything a bit more clear and to make it easier to see where and how I performed each step. I will preserve the code below, for now, just in case the notes I've put with it are of use to me at a later time. (1-4-2018)

Length Frequency

```
### 2013
(psd.13.freq20 <- xtabs(~lcat20,data=psd.13))
```

```
## lcat20
## 200 220 240 260 280 300 320 340 360 380 400 420
##   8   8   9   7   9  11   8  10  11  10   4   2
### calculate the percentage of the fish in each length nin
prop.table(psd.13.freq20)*100
```

```
## lcat20
##      200      220      240      260      280      300      320
## 8.247423 8.247423 9.278351 7.216495 9.278351 11.340206 8.247423
##      340      360      380      400      420
## 10.309278 11.340206 10.309278 4.123711 2.061856
```

```
### 2014
(psd.14.freq20 <- xtabs(~lcat20,data=psd.14))
```

```
## lcat20
## 200 220 240 260 280 300 320 340 360 380 400 420 460 480
##   1   3  16  28  17  13  10  22  12   6   7   2   2   1
### calculate the percentage of the fish in each length nin
prop.table(psd.14.freq20)*100
```

```
## lcat20
##      200      220      240      260      280      300
## 0.7142857 2.1428571 11.4285714 20.0000000 12.1428571 9.2857143
##      320      340      360      380      400      420
## 7.1428571 15.7142857 8.5714286 4.2857143 5.0000000 1.4285714
##      460      480
## 1.4285714 0.7142857

### 2015
(psd.15.freq20 <- xtabs(~lcat20,data=psd.15))

## lcat20
## 200 220 240 260 280 300 320 340 360 380 400 420 440 460
##   3   2   2   3   4   8  13   8   9   7   4   2   1   1

### calculate the percentage of the fish in each length bin
prop.table(psd.15.freq20)*100

## lcat20
##      200      220      240      260      280      300      320
## 4.477612 2.985075 2.985075 4.477612 5.970149 11.940299 19.402985
##      340      360      380      400      420      440      460
## 11.940299 13.432836 10.447761 5.970149 2.985075 1.492537 1.492537

### 2016
(psd.16.freq20 <- xtabs(~lcat20,data=psd.16))

## lcat20
## 200 220 240 260 280 300 320 340 360 380 400 420
##   5   8  10  15  14  12   7  12  13   6   2   2

### calculate the percentage of the fish in each length bin
prop.table(psd.16.freq20)*100

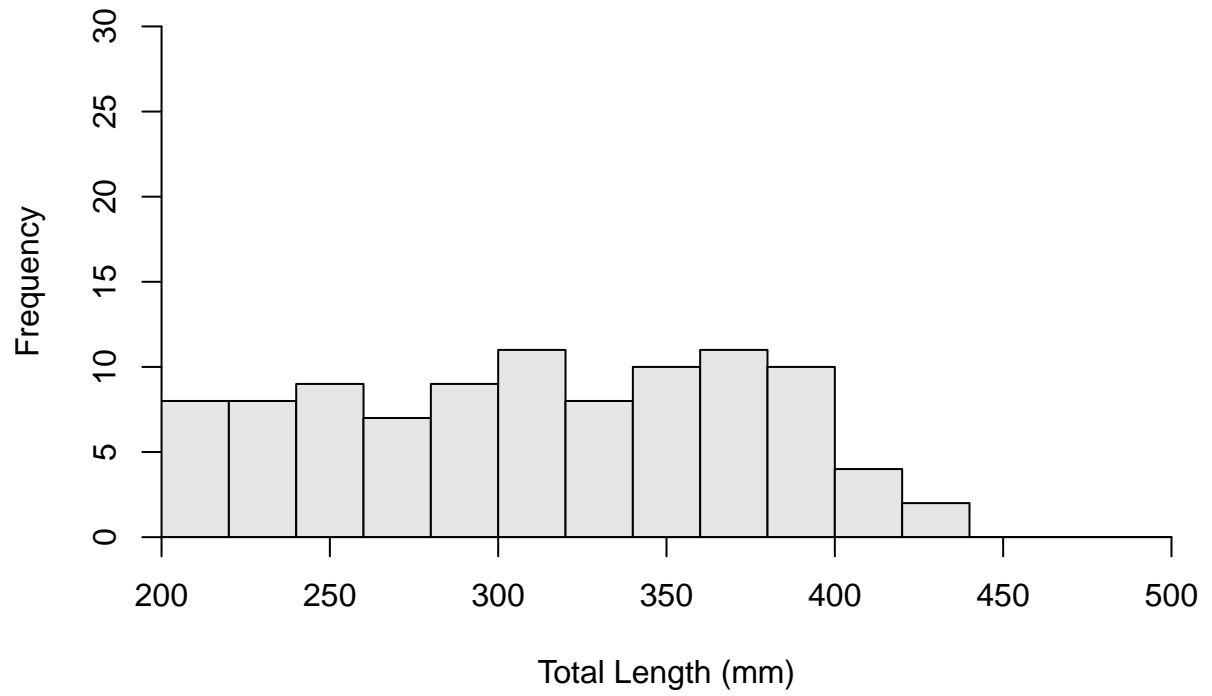
## lcat20
##      200      220      240      260      280      300      320
## 4.716981 7.547170 9.433962 14.150943 13.207547 11.320755 6.603774
##      340      360      380      400      420
## 11.320755 12.264151 5.660377 1.886792 1.886792
```

Lets view a quick histogram of the frequency of fish in each length bin.

```
par(mfrow=c(4,1)) ### arrange graphs 1 column 4 rows
par(mfrow=c(1,1)) ### reset to default

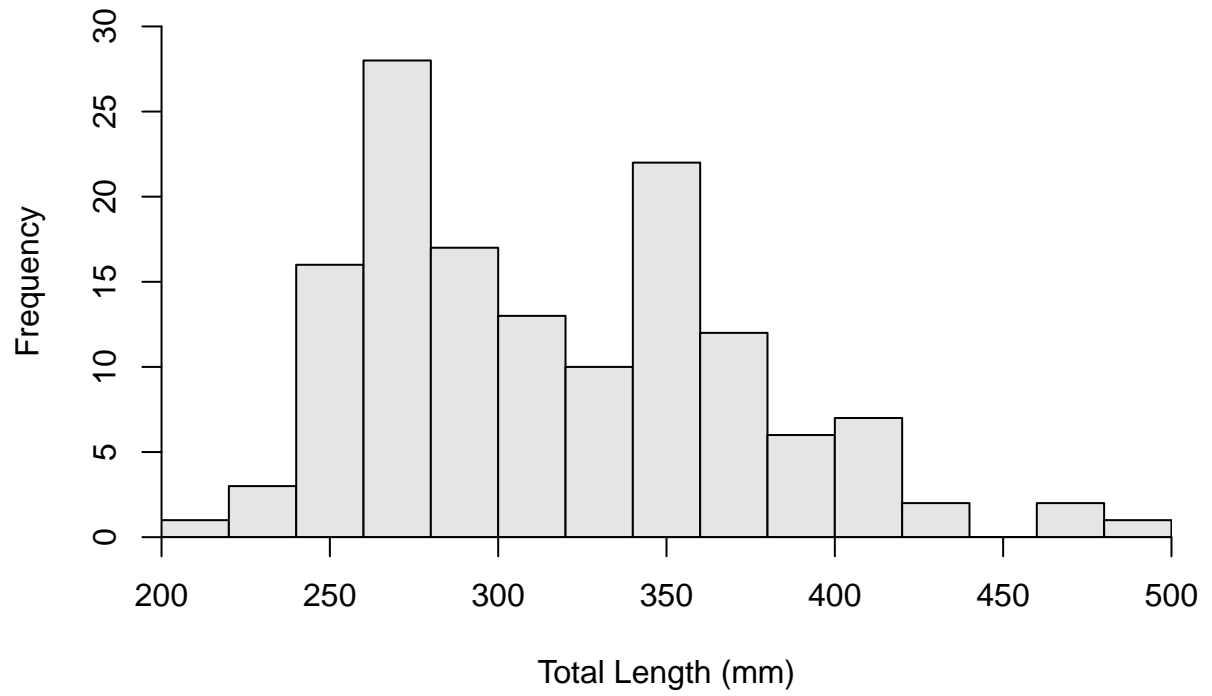
### 2013
hist(~Length,data=psd.13,
     breaks = seq(200,500,20),
     ylim=c(0,30),
     main="2014",
     xlab="Total Length (mm)")
```

2014



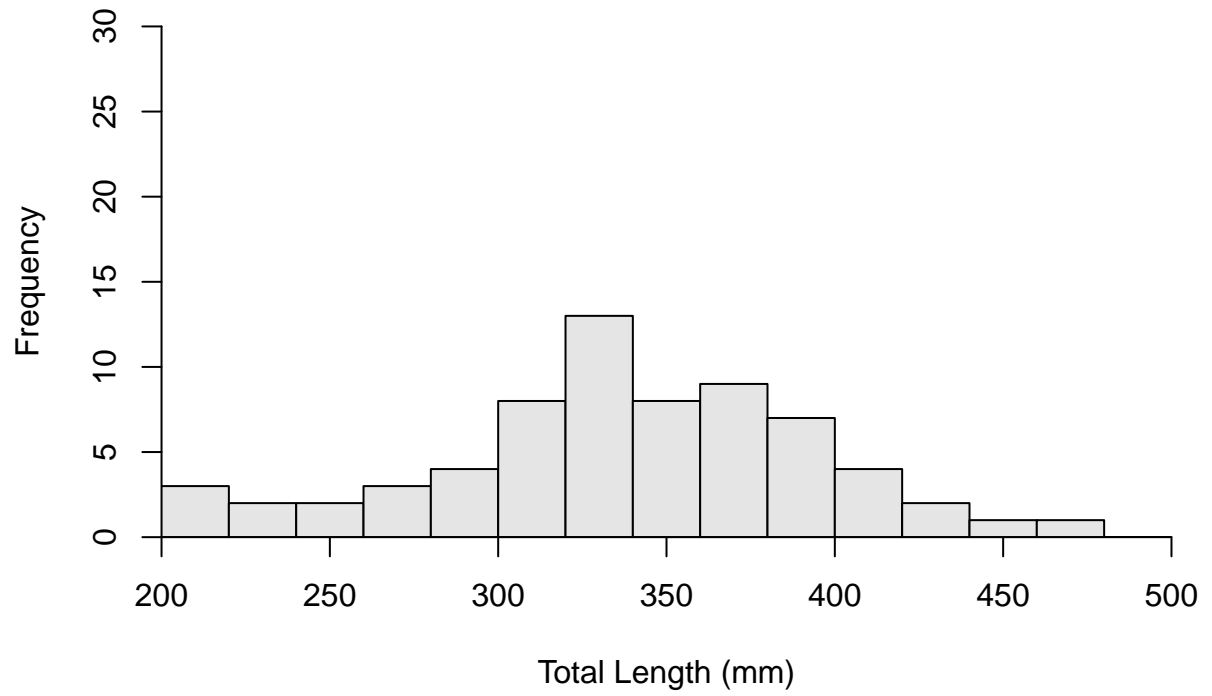
```
### 2014
hist(~Length,data=psd.14,
     breaks = seq(200,500,20),
     ylim=c(0,30),
     main="2014",
     xlab="Total Length (mm)")
```

2014



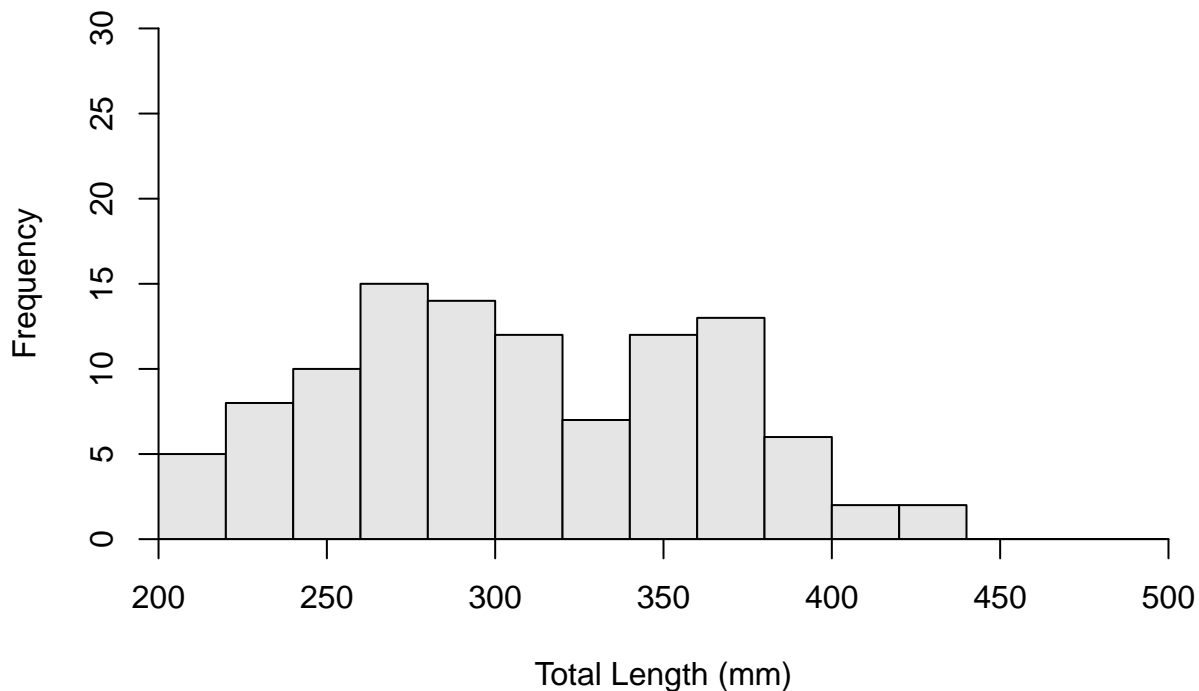
```
### 2015
hist(~Length,data=psd.15,
     breaks = seq(200,500,20),
     ylim=c(0,30),
     main="2015",
     xlab="Total Length (mm)")
```

2015



```
### 2016
hist(~Length,data=psd.16,
     breaks = seq(200,500,20),
     ylim=c(0,30),
     main="2016",
     xlab="Total Length (mm)")
```


2016



Based on the length frequency histograms above I would say that the largemouth bass population in lake Erie appears to be stable. The above graphs depict a even and gradual decrease in the number of individuals with length.

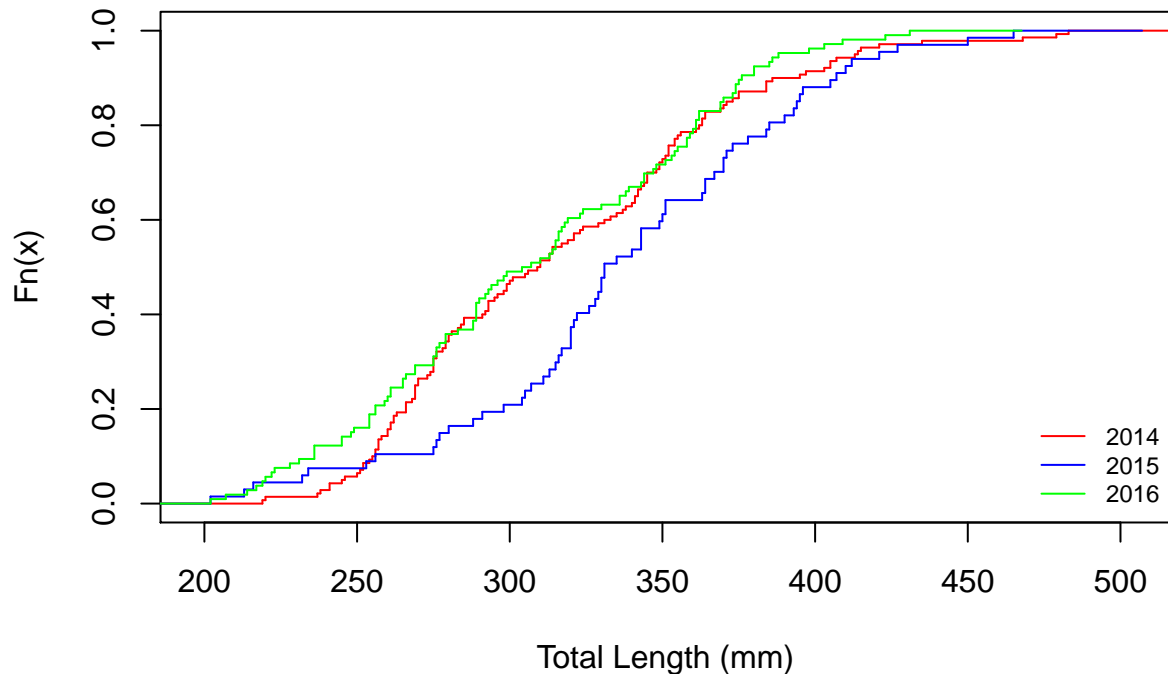
Cumulative Frequencies

Lets look at the empirical cumulative distribution function (ECDF). This is the proportion of fish less than each observed length. This should help me compare the length frequency distributions between years.

```
par(mfrow=c(1,1)) ### reset to default

### 2014
plot(ecdf(psd.14$Length),xlab="Total Length (mm)", do.points=FALSE,
     verticals=TRUE, main="", col.0line = NULL, col="red")
### 2015
plot(ecdf(psd.15$Length),xlab="Total Length (mm)", do.points=FALSE,
     verticals=TRUE, main="", col.0line = NULL, col="blue", add=T)
### 2016
plot(ecdf(psd.16$Length),xlab="Total Length (mm)", do.points=FALSE,
     verticals=TRUE, main="", col.0line = NULL, col="green", add=T)

legend("bottomright", c("2014","2015","2016"), col=c("red","blue","green"),
      lty=1, bty="n", cex=0.75)
```



```
(ks.ps <- c(ks.test(psd.14$Length,psd.15$Length)$p.value,
             ks.test(psd.15$Length,psd.16$Length)$p.value,
             ks.test(psd.14$Length,psd.16$Length)$p.value))
```

```
## Warning in ks.test(psd.14$Length, psd.15$Length): cannot compute exact p-
## value with ties
```

```
## Warning in ks.test(psd.15$Length, psd.16$Length): cannot compute exact p-
## value with ties
```

```
## Warning in ks.test(psd.14$Length, psd.16$Length): p-value will be
## approximate in the presence of ties
```

```
## [1] 0.002753545 0.002973292 0.478181287
```

```
(p.adjust(ks.ps))
```

```
## [1] 0.008260634 0.008260634 0.478181287
```

```
(diff.14.15 <- ks.test(psd.14$Length,psd.15$Length))
```

```
## Warning in ks.test(psd.14$Length, psd.15$Length): cannot compute exact p-
## value with ties
```

```
##
```

```
## Two-sample Kolmogorov-Smirnov test
```

```
##
```

```
## data: psd.14$Length and psd.15$Length
```

```
## D = 0.26962, p-value = 0.002754
```

```
## alternative hypothesis: two-sided
```

```
(diff.15.16 <- ks.test(psd.15$Length,psd.16$Length))
```

```
## Warning in ks.test(psd.15$Length, psd.16$Length): cannot compute exact p-
## value with ties
```

```
##
```

```
## Two-sample Kolmogorov-Smirnov test
##
## data: psd.15$Length and psd.16$Length
## D = 0.28161, p-value = 0.002973
## alternative hypothesis: two-sided
(diff.14.16 <- ks.test(psd.14$Length,psd.16$Length))

## Warning in ks.test(psd.14$Length, psd.16$Length): p-value will be
## approximate in the presence of ties

##
## Two-sample Kolmogorov-Smirnov test
##
## data: psd.14$Length and psd.16$Length
## D = 0.10836, p-value = 0.4782
## alternative hypothesis: two-sided
```

Looks like there is a significant difference in the length frequency distribution between years 2014 and 2015 ($D = 0.26962$, $P = 0.002754$), as well as the years 2015 and 2016 ($D = 0.27703$, $P = 0.003586$). However, there does not appear to be any difference between the length frequency distribution for the years 2014 and 2016 ($D = 0.10721$, $P = 0.4885$). The difference between length frequency found between year 2015 and 2014 or 2016 may be due to differences in the sites sampled or some other source of bias.?

Proportional Size Distribution (PSD)

Notes from Guy and Brown 9.5.2 Stock Density Indices

I will look at some size distribution indices in order to supplement the above length frequency analysis. I can use these to test for a correlation between size structure and other factors (However I only have 3 years of data). A question I should ask is whether the index value (size structure) reflects the density and dynamics of a fish population (Willis et al. 1993). As density increases PSD tends to decrease; declines in size structure can be attributed to slowing of growth and increased mortality as resources become scarce. However, a low PSD may also occur at low population densities due to overharvest or poor habitat (Guy and Brown CH9 pg 413).

As growth increases there is a tendency for PSD to increase. Low densities may result in high growth whereas high densities may result in slow growth (Guy and Brown CH9 pg 413).

Several studies have demonstrated that body condition is positively correlated with growth rate (See chapter 10 Guy and Brown). Individuals from low-density populations in which PSD is high tend to have high body condition values, and individuals from high-density populations in which PSD is low tend to have low body condition values. However body condition is an instantaneous measure, and slow growing fish may exhibit high body conditions at times of the year when food is abundant or when gonads are mature during the spawning period (Guy and Brown CH9 pg 413).

When total annual mortality increases there is a tendency for PSD to decrease. High mortality due to over-harvest and poor habitat also result in low PSD (Guy and Brown CH9 pg 414).

Predator and prey PSD are inversely related, however, the likelihood of this inverse relationship declines with the size of the water body. Carline et al. (1984) suggests that in Ohio impoundments, inverse relationships between size structure of largemouth bass and bluegill may not be expected in impoundments greater than 15 ha in size (Guy and Brown CH9 pg 414).

Note I may want to repeat these analysis using CPUE instead of individuals

Lets get started with PSD

Lets get started calculating Proportional Size Distributions (PSD). I mentioned earlier using the Preferred and Quality lengths, however, I think I will also look at the relative PSD of 457 mm fish preferred by anglers. This may not work though since I think these individuals are rare in my sample and perhaps absent in some years.

Lets start by looking at the frequency of fish in each gabelhouse length category.

```
#### 2014
(gfreq.14 <- xtabs(~gcat,data=psd.14))

## gcat
## preferred    quality    stock
##         18         57         65

#### Convert freq to percentage
(psdXY1.14 <- prop.table(gfreq.14)*100)

## gcat
## preferred    quality    stock
## 12.85714  40.71429  46.42857

(psdXY1.14.percent <- prop.table(gfreq.14)*100)

## gcat
## preferred    quality    stock
## 12.85714  40.71429  46.42857

#### 2015
(gfreq.15 <- xtabs(~gcat,data=psd.15))

## gcat
## preferred    quality    stock
##         15         38         14

#### Convert freq to percentage
(psdXY1.15 <- prop.table(gfreq.15)*100)

## gcat
## preferred    quality    stock
## 22.38806  56.71642  20.89552

#### 2016
(gfreq.16 <- xtabs(~gcat,data=psd.16))

## gcat
## preferred    quality    stock
##         10         44         52

#### Convert freq to percentage
(psdXY1.16 <- prop.table(gfreq.16)*100)

## gcat
## preferred    quality    stock
##  9.433962 41.509434 49.056604

#### I removed the *100 for calculation of psdXY1.YY b/c of Error
## given when computation CI about psdXY1.YY not being a table of proportions
#### I'll have to create a now prop table if I wat to see percent.
```

Note I may want to compare incremental PSD indices between years to look for changes in fish between Quality and Preferred length or preferred and Relative length of 457mm. I should research what the advantages

of incremental PSD indices are in greater detail first.

```
### first calculate the percentage of fish length x and above
### 2014
(psdX.14 <- cumsum(psdXY1.14))
```

```
## preferred    quality      stock
## 12.85714    53.57143    100.00000
```

```
### 2015
(psdX.15 <- cumsum(psdXY1.15))
```

```
## preferred    quality      stock
## 22.38806    79.10448    100.00000
```

```
### 2016
(psdX.16 <- cumsum(psdXY1.16))
```

```
## preferred    quality      stock
## 9.433962    50.943396    100.000000
```

I'm having a problem here and I'm not sure what is going on. The order of my variables (preferred, quality, stock) is given in alphabetical order and is opposite that in the book. Using `rcumsum` gives preferred PDS of 100. So I use `cume sum` which appears to work right. However, this is a problem when estimating the CI below. Maybe I just need to reverse the 0s and 1s in the `psdCI()` function. Meaning `psdCI(c(p,q,s))` instead of `psdCI(c(s,q,p))`.

```
### find the # of levels in gcat
levels(psd.14$gcat)
```

```
## [1] "preferred" "quality" "stock"
levels(psd.15$gcat)
```

```
## [1] "preferred" "quality" "stock"
levels(psd.16$gcat)
```

```
## [1] "preferred" "quality" "stock"
```

```
### 3 levels in gcat... so CI for PSD-Q = c(1,1,0), PSD-P = c(1,0,0) I think
```

```
### Make matrix of values to quickly compute CI for PSD-Q and PSD-P
(ivmat <- rbind("PSD-Q"=c(1,1,0),
               "PSD-P"=c(1,0,0)))
```

```
##      [,1] [,2] [,3]
## PSD-Q   1   1   0
## PSD-P   1   0   0
```

```
### 2014 #####
### Compute CI for multiple Indices
psdXY2.14 <- t(apply(ivmat,FUN = psdCI,MARGIN = 1,
                    ptbl=psdXY1.14,n=sum(gfreq.14),
                    method="multinomial"))
```

```
## Warning: 'ptbl' not a table of proportions; attempted to convert
## to proportions to continue.
```

```
## Warning: 'ptbl' not a table of proportions; attempted to convert
## to proportions to continue.
```

```
## Warning: Category sample size (18) <20, CI coverage may be lower than 95%.
```

```
colnames(psdXY2.14) <- c("Estimate", "95% LCI", "95% UCI")
psdXY2.14
```

```
##      Estimate 95% LCI 95% UCI
## PSD-Q      53.6   43.3   63.9
## PSD-P      12.9    5.9   19.8
```

```
### Individual PSD indices
```

```
psdCI(c(1,1,0),ptbl=psdXY1.14, n=sum(gfreq.14), method = "binomial",
      label = "PSD-Q")
```

```
## Warning: 'ptbl' not a table of proportions; attempted to convert
## to proportions to continue.
```

```
##      Estimate 95% LCI 95% UCI
## PSD-Q      53.6   45.3   61.6
```

```
### Not sure what is going on here the estimate form the CI is different than the estiamte in psdx.14
```

```
### Reversing 0s and 1s fixed this... psdCI(c(p,q,s)) instead of psdCI(c(s,q,p))
```

```
### Also getting the warning below
```

```
### Warning message:
```

```
### 'ptbl' not a table of proportions; attempted to convert
### to proportions to continue.
```

```
psdCI(c(1,0,0),ptbl=psdXY1.14, n=sum(gfreq.14), method = "binomial",
      label = "PSD-P")
```

```
## Warning: 'ptbl' not a table of proportions; attempted to convert
## to proportions to continue.
```

```
##      Estimate 95% LCI 95% UCI
## PSD-P      12.9    8.3   19.4
```

```
### 2015 #####
```

```
### Compute CI for multiple Indices
```

```
psdXY2.15 <- t(apply(ivmat,FUN = psdCI,MARGIN = 1,
                    ptbl=psdXY1.15,n=sum(gfreq.15),
                    method="multinomial"))
```

```
## Warning: 'ptbl' not a table of proportions; attempted to convert
## to proportions to continue.
```

```
## Warning: 'ptbl' not a table of proportions; attempted to convert
## to proportions to continue.
```

```
## Warning: Category sample size (15) <20, CI coverage may be lower than 95%.
```

```
colnames(psdXY2.15) <- c("Estimate", "95% LCI", "95% UCI")
psdXY2.15
```

```
##      Estimate 95% LCI 95% UCI
## PSD-Q      79.1   66.9   91.3
## PSD-P      22.4    9.9   34.9
```

```
### Individual PSD indices
```

```
psdCI(c(1,1,0),ptbl=psdXY1.15, n=sum(gfreq.15), method = "binomial",
      label = "PSD-Q")
```

```
## Warning: 'ptbl' not a table of proportions; attempted to convert
## to proportions to continue.
```

```

##          Estimate 95% LCI 95% UCI
## PSD-Q      79.1    67.9    87.1
psdCI(c(1,0,0),ptbl=psdXY1.15, n=sum(gfreq.15), method = "binomial",
      label = "PSD-P")

## Warning: 'ptbl' not a table of proportions; attempted to convert
## to proportions to continue.

##          Estimate 95% LCI 95% UCI
## PSD-P      22.4    14.1    33.7
#### 2016 #####
#### Compute CI for multiple Indices
psdXY2.16 <- t(apply(ivmat,FUN = psdCI,MARGIN = 1,
                    ptbl=psdXY1.16,n=sum(gfreq.16),
                    method="multinomial")))

## Warning: 'ptbl' not a table of proportions; attempted to convert
## to proportions to continue.

## Warning: 'ptbl' not a table of proportions; attempted to convert
## to proportions to continue.

## Warning: Category sample size (10) <20, CI coverage may be lower than 95%.
colnames(psdXY2.16) <- c("Estimate", "95% LCI", "95% UCI")
psdXY2.16

##          Estimate 95% LCI 95% UCI
## PSD-Q      50.9    39.1    62.8
## PSD-P       9.4     2.5    16.4
#### Individual PSD indices
psdCI(c(1,1,0),ptbl=psdXY1.16, n=sum(gfreq.16), method = "binomial",
      label = "PSD-Q")

## Warning: 'ptbl' not a table of proportions; attempted to convert
## to proportions to continue.

##          Estimate 95% LCI 95% UCI
## PSD-Q      50.9    41.6    60.3
psdCI(c(1,0,0),ptbl=psdXY1.16, n=sum(gfreq.16), method = "binomial",
      label = "PSD-P")

## Warning: 'ptbl' not a table of proportions; attempted to convert
## to proportions to continue.

##          Estimate 95% LCI 95% UCI
## PSD-P       9.4     5.2    16.5

  Lets try the other way of calculating CI for PSD.
#### 2014
## Traditional
psdCI.14 <- psdCalc(~Length,data=psd.14,species = "Largemouth Bass",what="traditional")

## Warning: Some category sample size <20, some CI coverage may be
## lower than 95%.

```

```
## Incremental
psdCalc(~Length,data=psd.14,species = "Largemouth Bass",what="incremental")

## Warning: Some category sample size <20, some CI coverage may be
## lower than 95%.

##      Estimate 95% LCI 95% UCI
## PSD S-Q      46      36      57
## PSD Q-P      41      31      51
## PSD P-M      13       6      20

### 2015
## Traditional
(psdCI.15 <- psdCalc(~Length,data=psd.15,species = "Largemouth Bass",what="traditional"))

## Warning: Some category sample size <20, some CI coverage may be
## lower than 95%.

##      Estimate 95% LCI 95% UCI
## PSD-Q        79      67      91
## PSD-P        22      10      35

## Incremental
psdCalc(~Length,data=psd.15,species = "Largemouth Bass",what="incremental")

## Warning: Some category sample size <20, some CI coverage may be
## lower than 95%.

##      Estimate 95% LCI 95% UCI
## PSD S-Q      21       9      33
## PSD Q-P      57      42      72
## PSD P-M      22      10      35

### 2016
## Traditional
psdCalc(~Length,data=psd.16,species = "Largemouth Bass",what="traditional")

## Warning: Some category sample size <20, some CI coverage may be
## lower than 95%.

##      Estimate 95% LCI 95% UCI
## PSD-Q        51      39      63
## PSD-P         9       2      16

## Incremental
psdCalc(~Length,data=psd.16,species = "Largemouth Bass",what="incremental")

## Warning: Some category sample size <20, some CI coverage may be
## lower than 95%.

##      Estimate 95% LCI 95% UCI
## PSD S-Q      49      37      61
## PSD Q-P      42      30      53
## PSD P-M       9       2      16
```

Compare PSD between Years

See Introductory Fisheries Analysis with R 6.4 pg 122